

**Exhibit 2: ClustalW (Amino Acid) Alignment**

CLUSTAL W 2.0 multiple sequence alignment

Sequence format is Pearson  
number of seqs is: 2  
Sequence 1: SEQ147 311 aa  
Sequence 2: T\_petrophila 312 aa

comparing  
paramArg [setSeqNoRange] = off  
comparing

Start of Pairwise alignments

Sequences (1:2) Aligned. Score: 95  
Guide tree file created: [/ebi/extserv/clustalw-  
work/interactive/2007122119/clustalw2-20071221-19204050.dnd]

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-  
work/interactive/2007122119/clustalw2-20071221-19204050.aln]

SEQ148	MNDLIRKYAKDQLETLKRIIEKSEGISILINGEDLSYPREVSLELPEYVEKFPPKASDVL	60
T_petrophila	MNDLIRKYAKDQLEILKRIIEKSEGISILINGEDLSYPREVSLELPEYVEKFPPKASDVL	60
	*****	*****
SEQ148	EIDPEGENIGIDDIRTIKDFLNYSPELYTRKYVIVHDCERMTQQAANAFLKALEEPPEYA	120
T_petrophila	EVDPEEENIGIDEIRTIKDFLNYSPELYTRKYVIVHDCERMTQQAANAFLKTLEEPPEYA	120
	*, ****	*****;
SEQ148	VIVLNTRRWHYLLPTIKSRVFRVVNVPKEFRDLVKEKIGDWEELPLLERDFKTALEAY	180
T_petrophila	VIVLNTRRWHYLLPTIKSRVFRVVNVPKEFRDLVKEKIGDFWEELPLLERDFKTAFEAY	180
	*****;	*****;
SEQ148	KLGAEKLSGLMESLKVLTEKLLKKVLSKGLEGYLACRELLERFSKVESKEFFALFDQVT	240
T_petrophila	KLGAEKLSGLMESLKVLTEKLLKKALSEGLEGYLACRELLERFSKVESKEFFALFDQLT	240
	*****;	*****;
SEQ148	NTITGKDAFLLIQRLTRIILHENTWESVED-KSVSFLDSILRVKIANLNNKLTLMNILAI	299
T_petrophila	NTITGKDSFLLIQRLTRIVLHENTWESVEDQKSVSFLDSILRVKIANLNNKLTLMNILAI	300
	*****;	*****;
SEQ148	HRERKRGVNAWS 311	
T_petrophila	HRERKRGVNAWS 312	
	*****	